Carimas 2.4 (Core)

User's Guide

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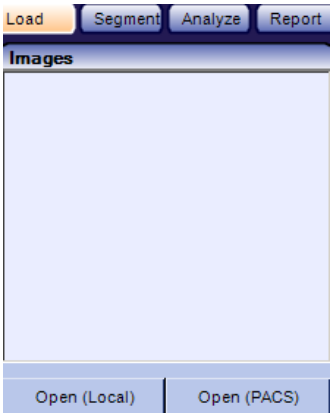
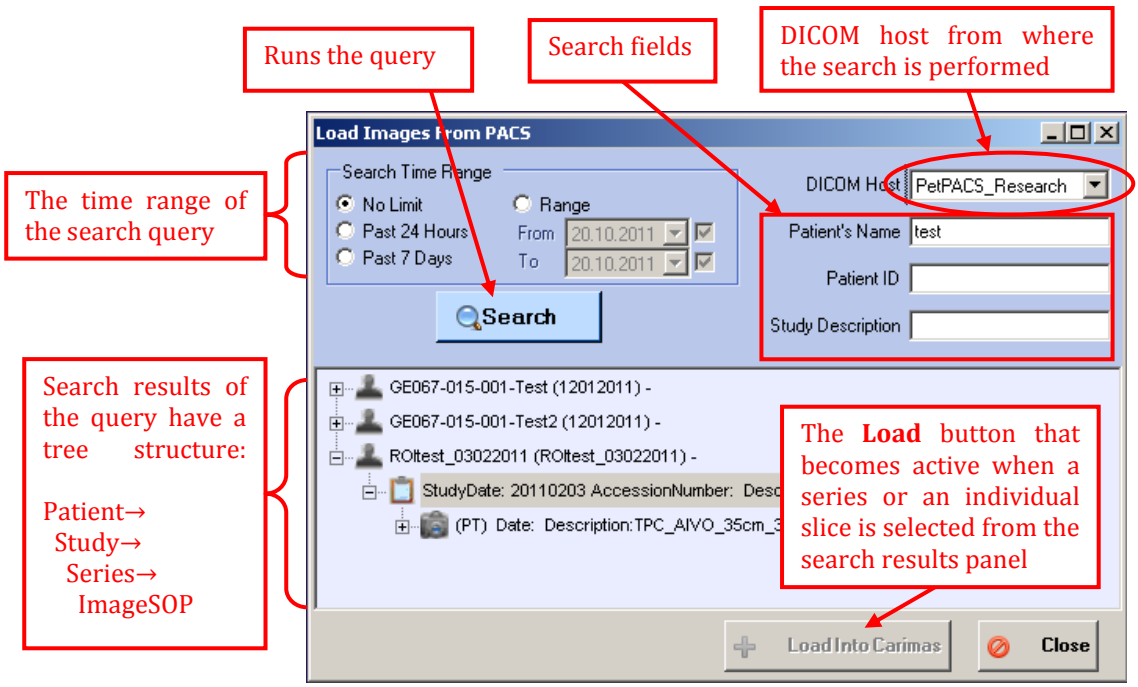
1 Loading images to Carimas

Once you have opened Carimas you are presented with the **Load** panel, which invites you to load images either from your local drives – **Open (Local)**, or from picture archiving and communication system (PACS) available at your institution – **Open (PACS)**.



1.1. Loading from PACS

Carimas has a separate dialog box for PACS communication. You can open it by clicking the **Open (PACS)** button.



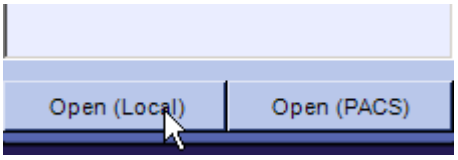
The search follows five steps:

1. Select target DICOM host + search fields + time range
2. Click **Search**

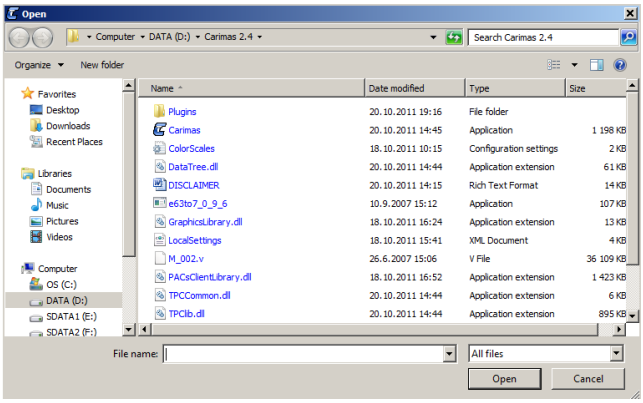
3. Select correct series or individual slice from search results panel
4. Click the **Load into Carimas** button that becomes active when series or slice is selected
5. The image has been loaded into Carimas. Load more images the same way or click the **Close** button.

1.2. Loading from a local disk

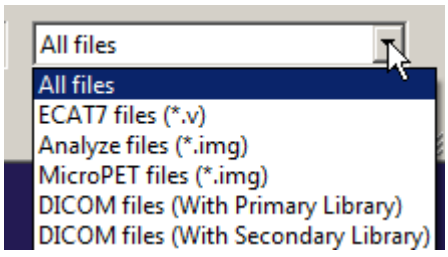
To open images on local drives click the **Open (Local)** button:



The standard **Open File** dialog box will appear; you can load images of all formats supported in TPClib.



For DICOM there is also an alternative option: the Secondary Library, which can be selected from the format drop-down list.

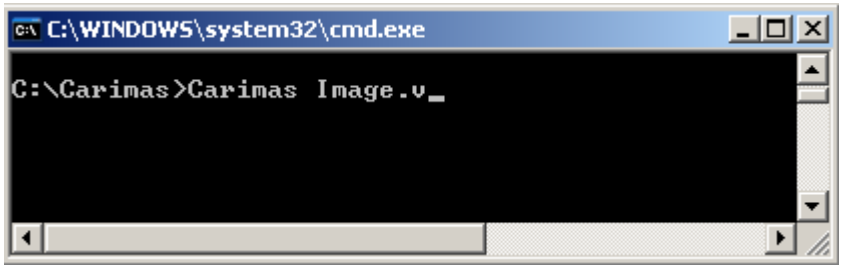


Images loaded with the Secondary Library will consume fewer resources.

Local opening always opens entire image series, not individual slices. So, in DICOM, by selecting and clicking on one file only, Carimas will automatically load the rest slices of the series consisting of many files like DICOM.

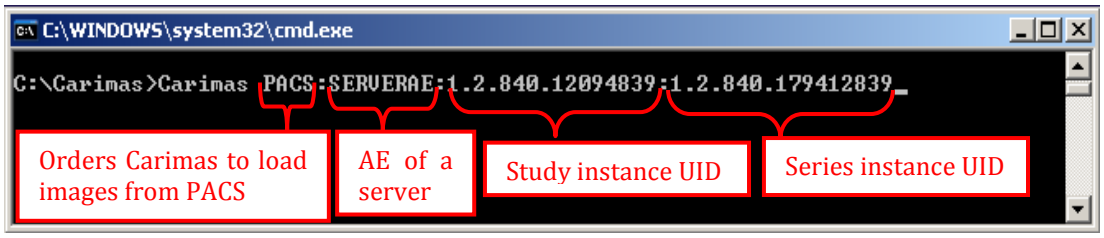
1.3. Loading from a command line

Images can be opened also from command line by giving full path to the image. In DICOM case there are two options: full path to one slice and Carimas will open the remaining slices as well or give only folder containing the DICOM slices.



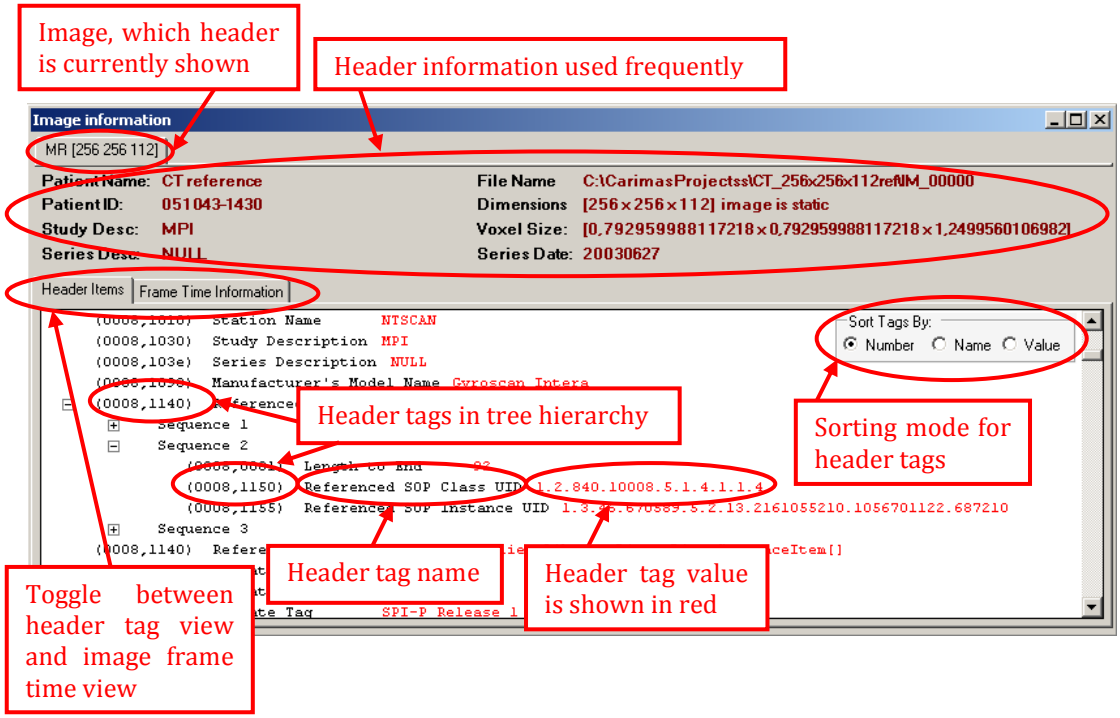
Images on PACS can also be opened from command line with parameter with following syntax:

```
PACS:SERVER_AE:StudyInstanceUID:SeriesInstanceUID.
```



1.4 Viewing the image header

A header of a loaded image can be seen from menu: View→Header or clicking image from image list and selecting “Show image header”. Following dialog is shown:

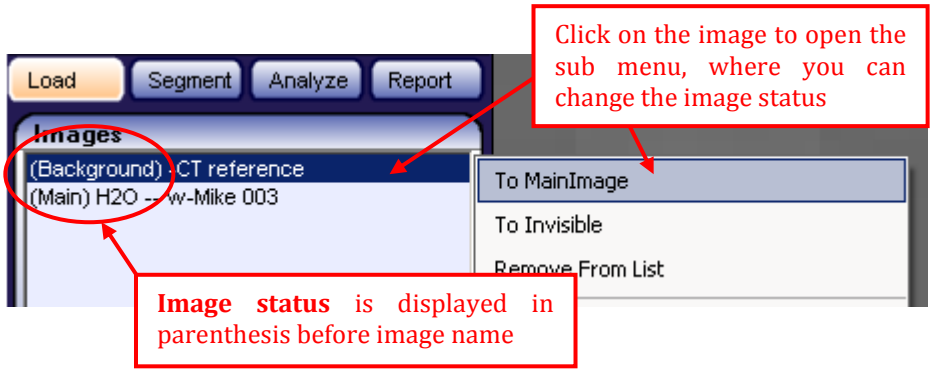


The image frame time view lists start, mid, end and duration values for each frame.

1.5 Preparing loaded images for visualization

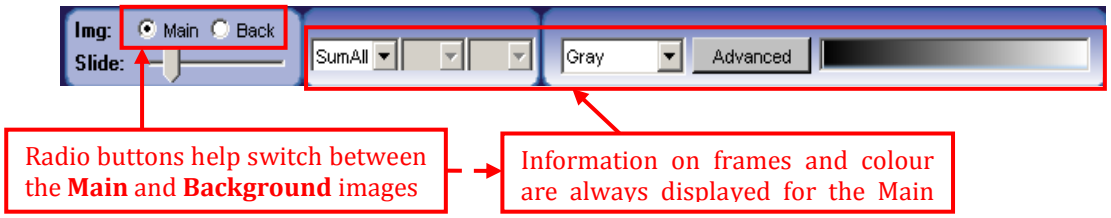
1.5.1 Main and Background images

The loaded image in Carimas can be in four qualities: main, invisible, background and selected (either main or background). Simultaneously you can visualize two images at maximum. One will always be the **Main** image and the other – the **Background** image.

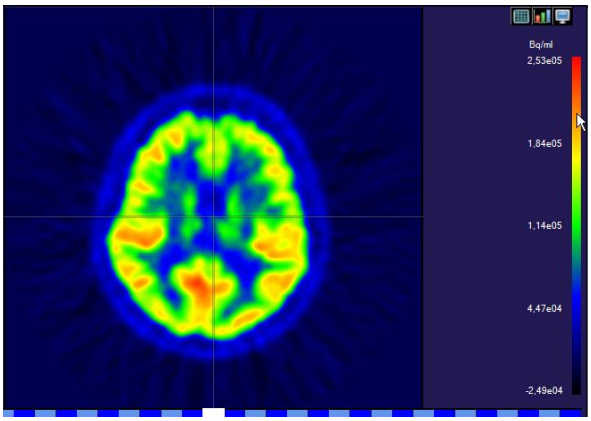


1.5.2 *The Selected image*

The Selected image is either the main image or the background one. This selection will define the display of colour and frame options.

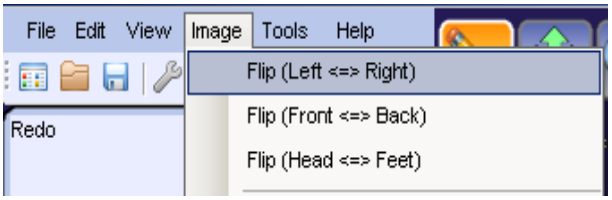


Also, the colour bar on the right side of all the four windows is the bar for the selected image.



1.5.3 *Flipping image data*

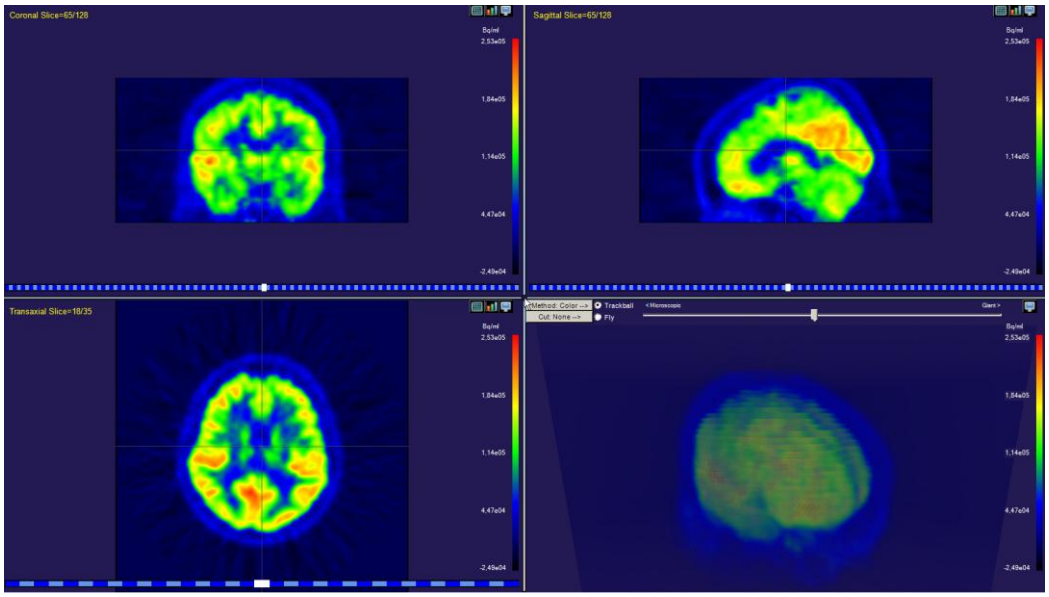
If image opens in wrong orientation, image data can be flipped from Image menu. Flips are flipping the currently **selected image** (see selected image chapter). It is good to check the flips before drawing any ROI's because flips affect only to selected image, not to ROIs.



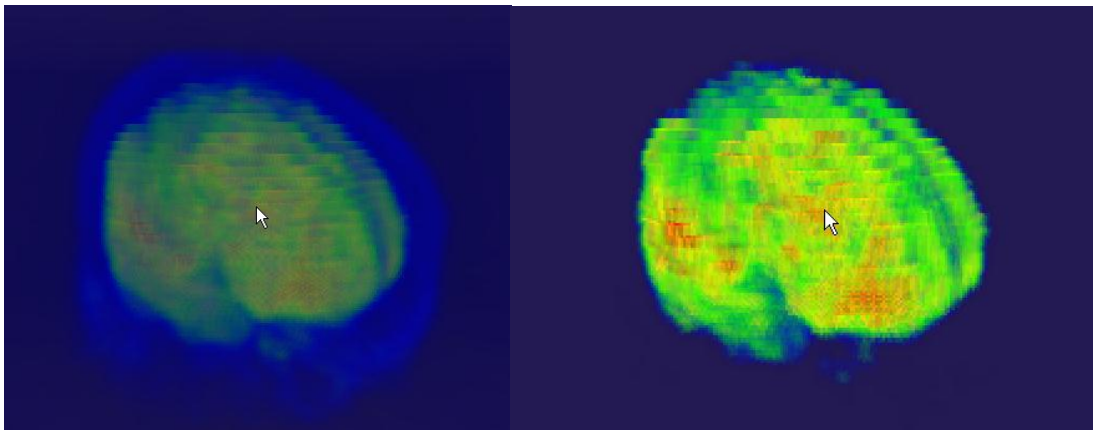
2 Visualization

2.1 Interacting with graphical windows

When you have an image loaded, it is centred to all windows so that it is fully visible.



The camera of 3D window is placed so that it shows the whole image, thus the general look of the image can be easily seen by rotating the 3D camera around. Normally the start and end colour bar values need to be adjusted for getting good 3D visualization.

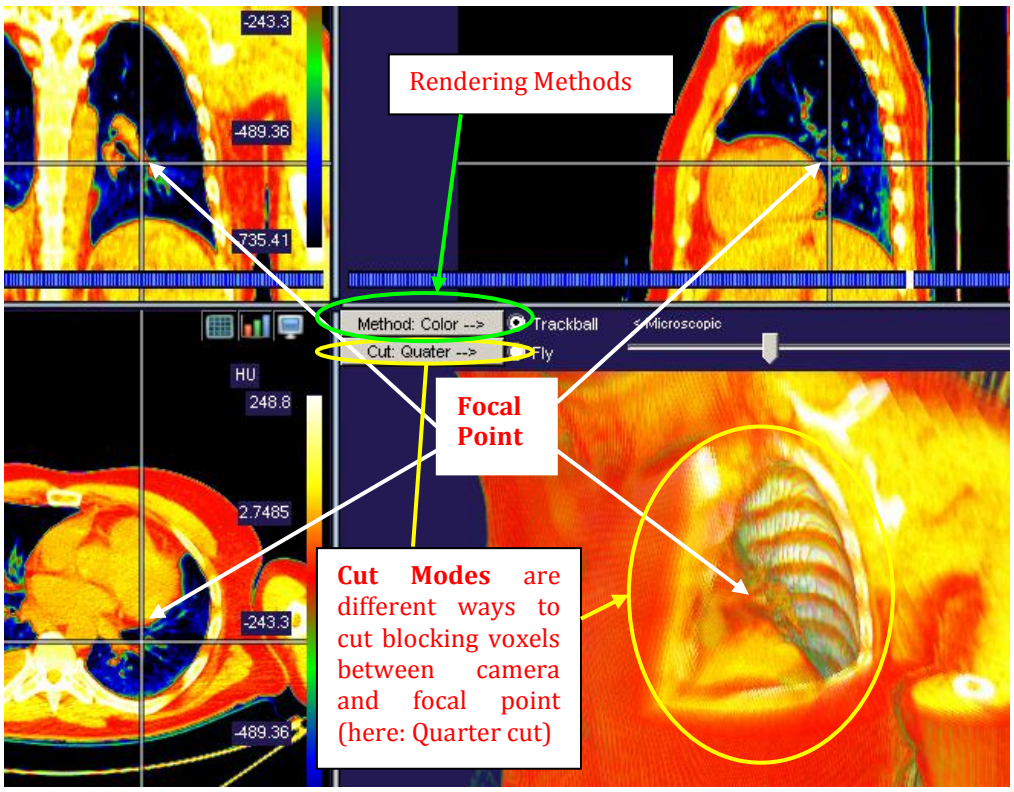


2.2 Focal point and screens

There is always one 3D focal point which is the basis for all visualization windows. When image is loaded, this focal point is automatically set to a centre of the loaded image. All 2D windows have grey horizontal and vertical

lines which cross at the focal point. 3D window is centred to this point so that the rotations will be around it and zoom will be towards it. Slice positions of 2D windows are also calculated from this point.

Focal point can be moved in the Cut mode (shortcut is the **Alt** key + a mouse click) or dragging the mouse in 2D windows. In the 3D window double clicking on a voxel will set focal point on it. Also the Move tool of 3D window moves the focal point.



2.3 Visualizing smaller part of image with 3D window

If some small part of the image needs to be visualized, the easiest way is to move the focal point cross of 2D windows to centre of the area of interest. Then the centre of 3D window always points towards area of interest. After this it's easy to zoom and rotate 3D camera around area of interest.

2.4 Cut modes

Usually the smaller regions are inside the image so that other voxels are between camera and area of interest, blocking the view. Cut methods are methods for making these blocking voxels invisible. Cut modes are found from top left corner of 3D window.

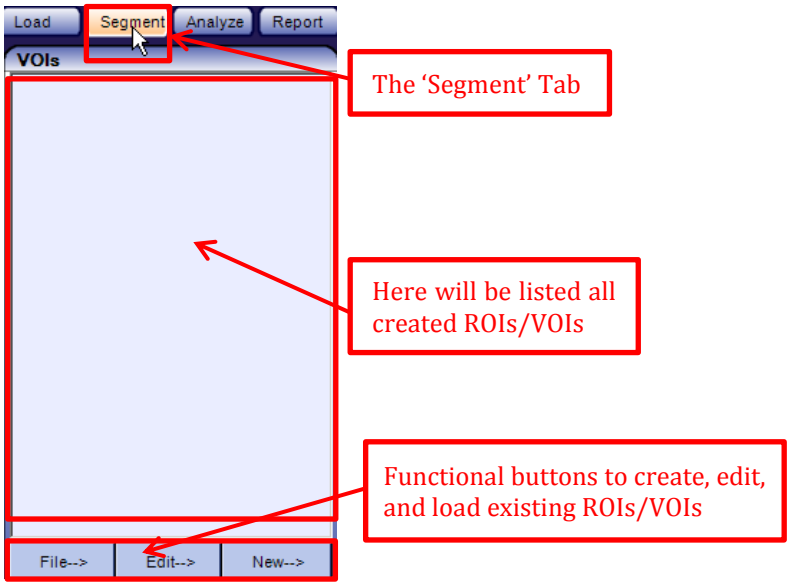
2.5 Custom 2D slice directions instead of tansaxial, coronal and sagittal

By default Carimas visualizes all images in transaxial, sagittal and coronal 2D windows (**Projection View**). It is also possible to define custom slice directions for 2D visualization. Custom slice directions are defined with 3D camera and the three 2D window cuts will be: Camera right, Camera top and Camera back. 2D visualization mode is changed from menu: **View → Camera View**.

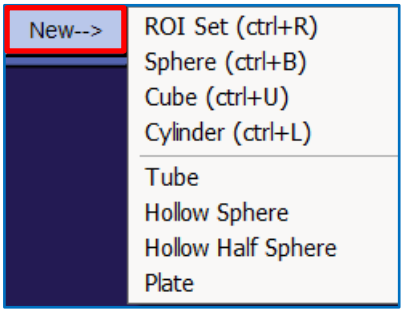
3 Segmentation of loaded images

Image segmentation – "the process of classifying the voxels of an image into a set of distinct classes" (Zaidi and El Naqa, 2010)[1]

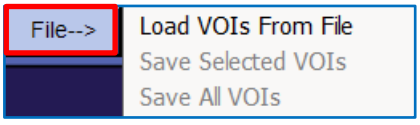
Click the **Segment** tab to enable the segmentation of the loaded image(s).



Click the **New** button to create a ROI Set or a VOI; select the option you need.



Click the **File** button to load the existing set of ROIs or VOIs:



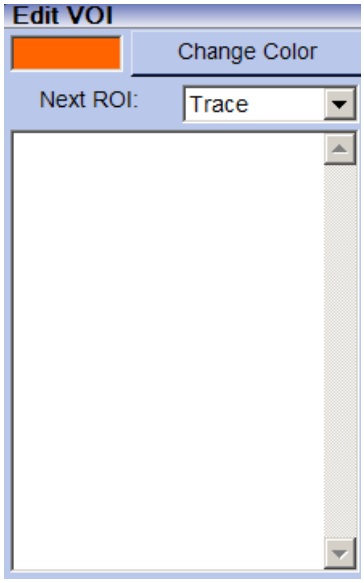
[1]NB: "Medical image segmentation has been identified as the key problem of medical image analysis and remains a popular and challenging area of research <…>. The difficulty in PET image segmentation is compounded by the low spatial resolution and high noise characteristics of PET images…" (Zaidi and El Naqa, 2010)

Creating VOIs from primitives might be a fast way and the only one needed in case of more or less simply shaped volumes (some tumors, bone sequestra, etc.); if the volume of your interest is a complicated one, you might prefer drawing ROIs in every plane and then combine the ROI set into a VOI. Carimas will give you a lot of freedom in this matter.

Click on any option from the **New** list and the **Edit VOI** panel appears.

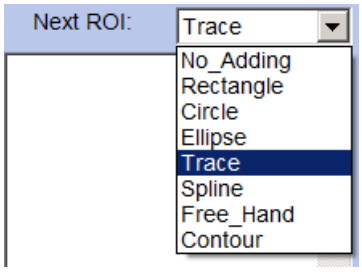
3.1 ROI lists

Clicking on ROI Set will open this variant of **Edit VOI** panel.

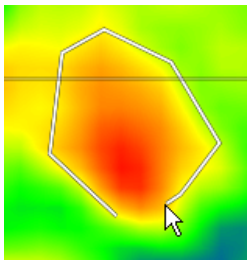


3.1.1 Selecting type of ROI

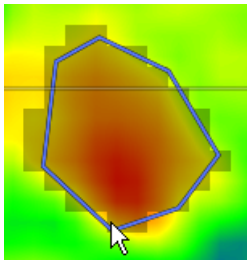
Click on **Next ROI** drop-down list and select which ROI you want to draw.



Trace is the default one; with it you create polygonal ROIs. Left-click mouse to set angles, drag it to draw a side.

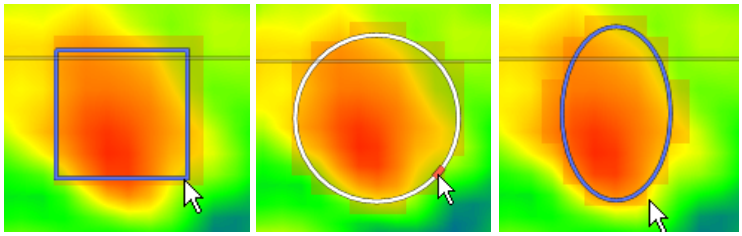


To close the drawn ROI drag towards the starting point.

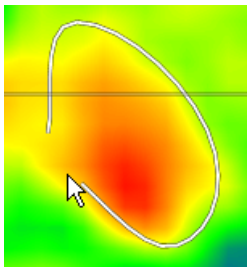


The drawn ROI shows you the voxels that will be included in the analysis.

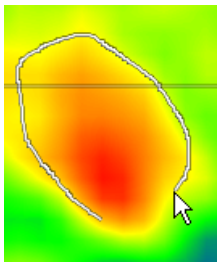
Drawing **Rectangle**, **Circle** and **Ellipse** is straightforward and can be done with one left click and dragging the resulting ROIs to the needed size:



Drawing Spline ROI every left click gives a new bend; closing is the same as with the Trace.

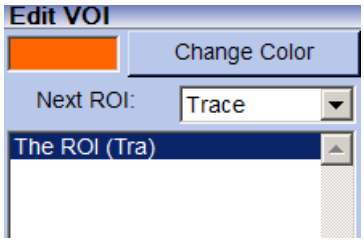


With Freehand you draw by dragging the mouse; releasing the left button will close the ROI no matter where in image you released the button.



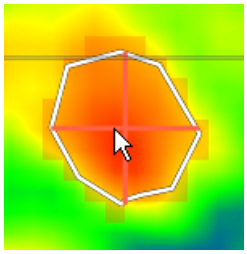
3.1.2 *ROI modify controls*

To modify geometry of the created ROI select it in the Edit VOI panel

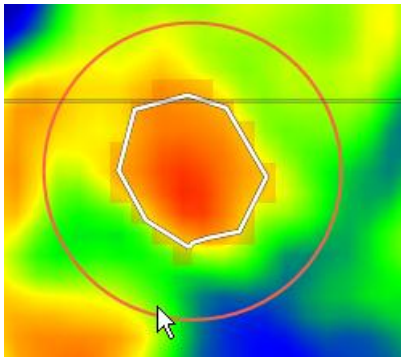


Going through the following pictures, note the position of the cursor: its position relative to the ROI determines how you can modify the geometry of the ROI.

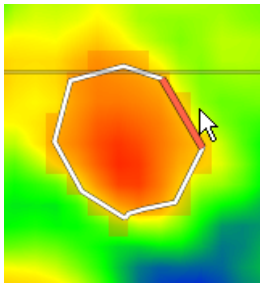
To move the ROI place the cursor in the centre, see the red intersection appear, drag in the needed direction:



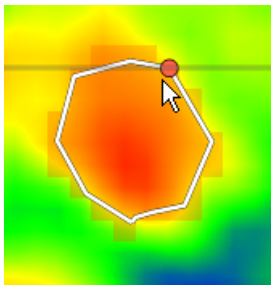
To rotate the ROI around its imaginative centre, move the cursor outside ROIs borders, see the red circle appear, drag as needed.



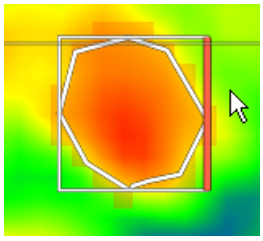
To move a side of the ROI and modify its position and adjacent sides as well as ROI's area, move the cursor close to it and drag:



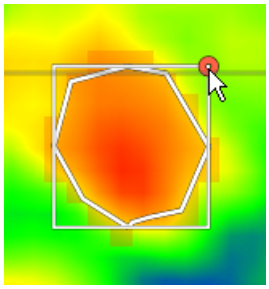
Move cursor to an angle and drag it:



Selecting the outer side will modify the ROI in the direction of the side: you can stretch or shrink the ROI:



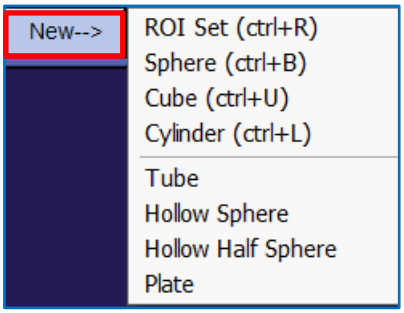
Selecting and dragging one of the angles of the outer ROI box will enlarge or shrink the whole ROI depending on the direction of the move:



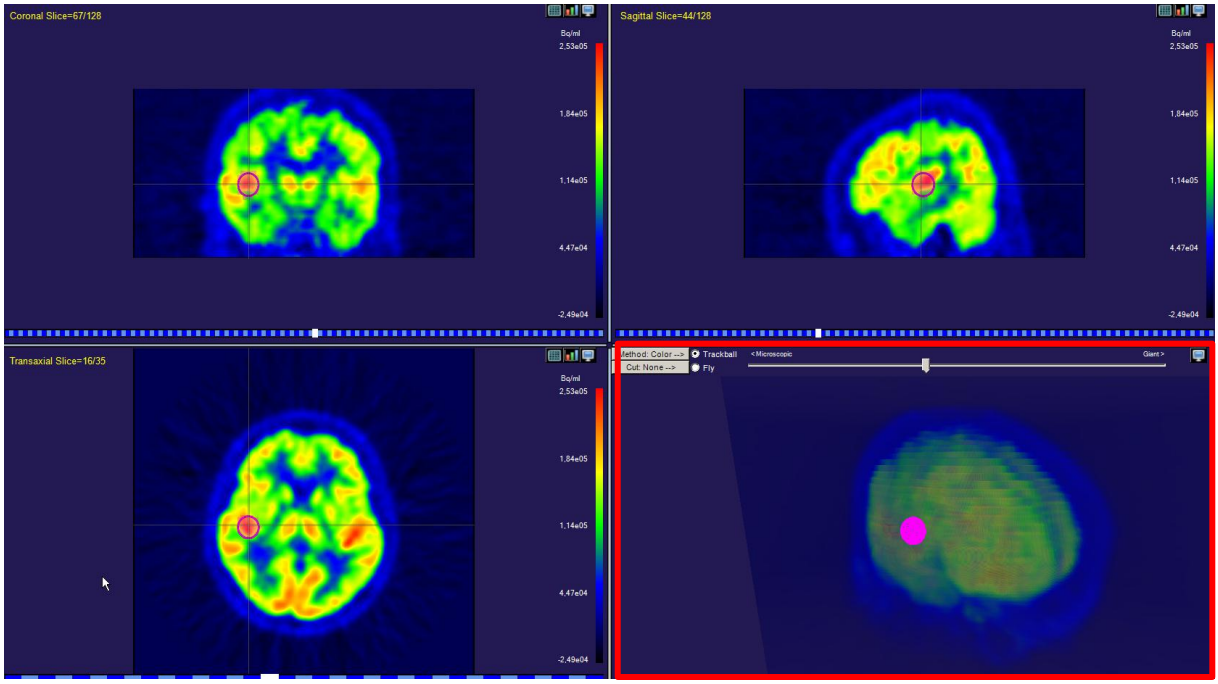
3.2 3D VOIs

3.2.1 Adding a 3D shape

Click the **New** button to create a VOI; select the option you need.

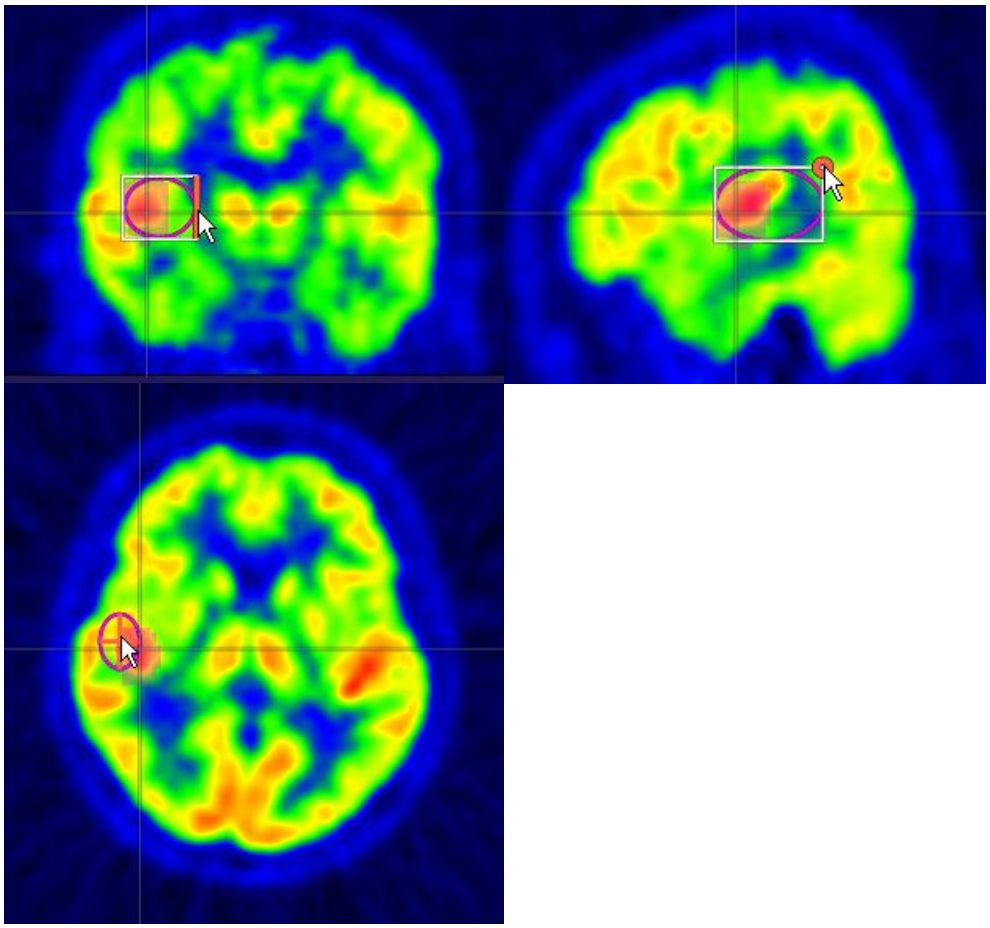


As you are creating a 3D object, you will see its projections in all three images projections; the VOI itself is best visible in the 3D window (here we created a **Sphere**):

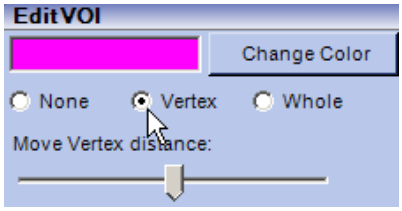


3.2.2 Editing

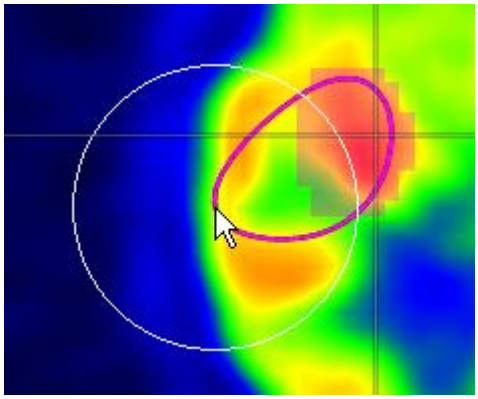
In any of the projections you can modify VOI projections the same way as ROIs:



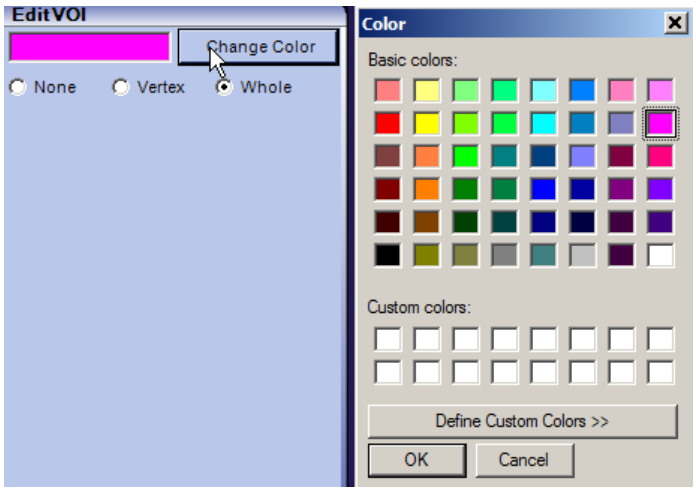
You can also use **Vertex** – the moulding tool for fine changes:



On the slider fix the size of the Vertex (small size grows from left to right); select the part you want to mould and drag in the needed direction:



Clicking on the **Change Color** button, you can select and change the colour of the VOI:

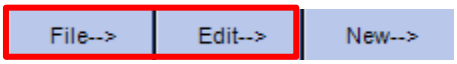


3.2.3 Using VOI filters

You can use several **VOI Filters** from the **Tools** Menu.

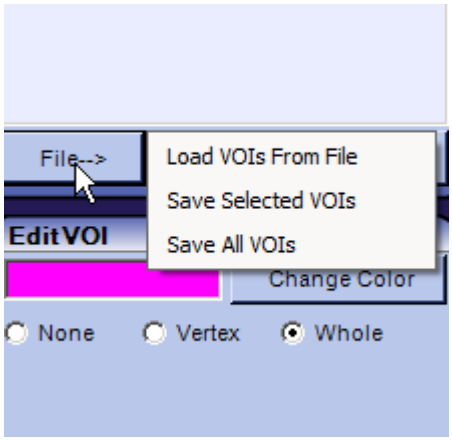
3.3 Tools for all ROIs/VOIs

The File and Edit buttons help you save, load and modify the ROIs/VOIs you created:

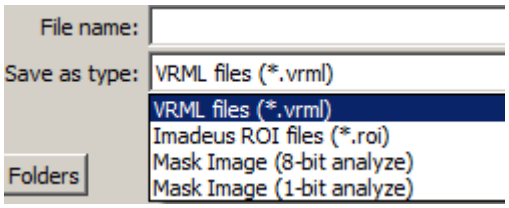


3.3.1 The File button options

Clicking the **File** button you can choose to load already existing VOIs or save the created ones. Carimas offers you options to save all the VOIs – **Save All VOIs**, or only selected ones – **Save Selected VOIs.**

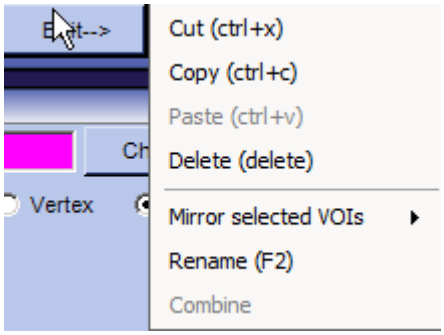


When saving the VOIs you have options of the saving format.

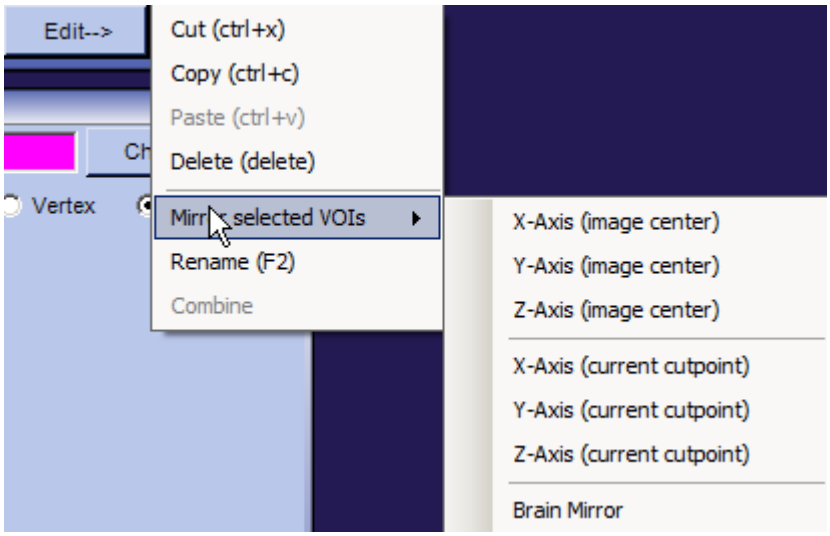


3.3.2 The Edit button options

The **Edit** button offers you to perform all general functions on your ROI/VOI such as **Cut**, **Copy**, **Paste**, **Delete** and **Rename**.



Selecting **Mirror selected VOIs** lets you create new VOIs, associated with the existing ones, without much effort.

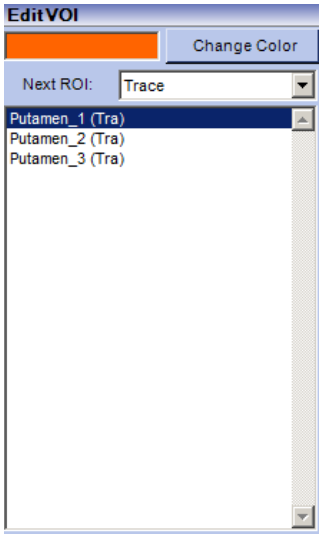


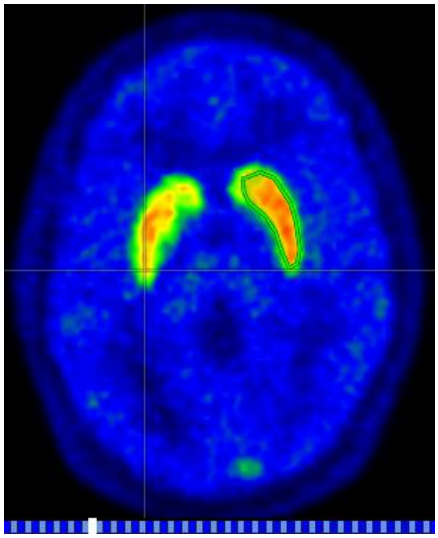
4 Analysis of segmented regions

Images we analyse roughly are either static or dynamic; as the name implies, the critical difference between them is a time dimension. Static (akin to a photo picture) will have one frame, dynamic (akin to a video) will have more than one frame. Analysis pathways of static and dynamic images differ.

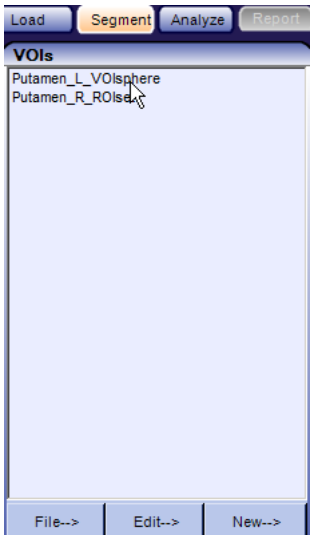
4.1 Static image analysis

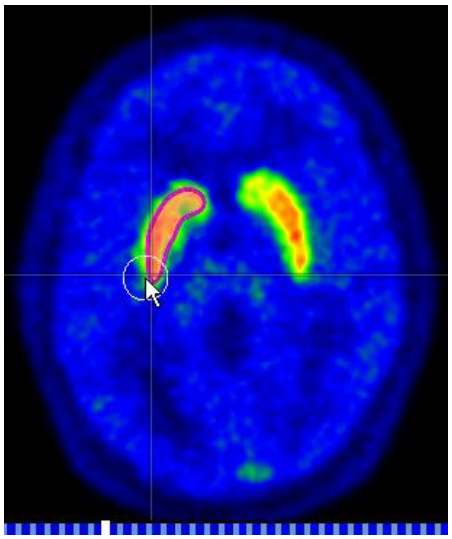
In the analysed image the ROI Set, consisting of three ROIs, has been drawn in the right putamen:



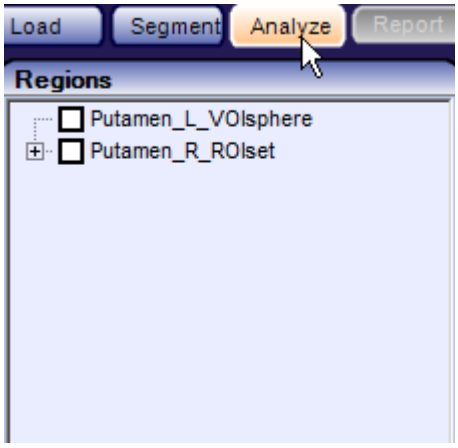


The spherical VOI has been created, placed into the region of the left putamen and moulded in three projections with the Vertex tool to assume the shape of the putamen:

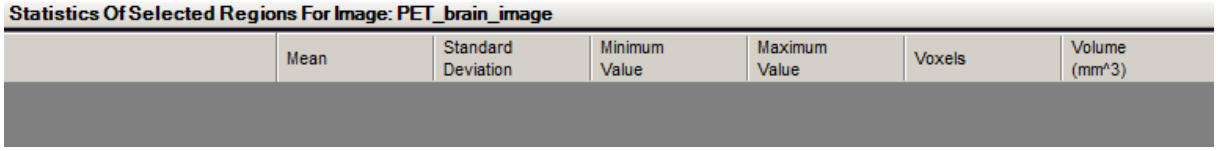




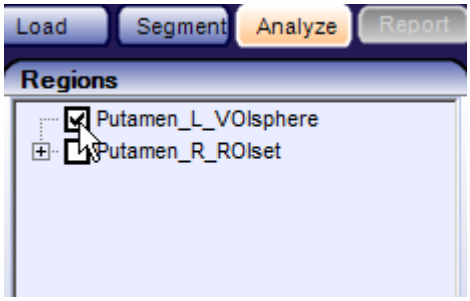
Click the **Analyse** tab to enter the analysis mode. In the **Regions** panel you see all VOIs and ROIs present in the image.



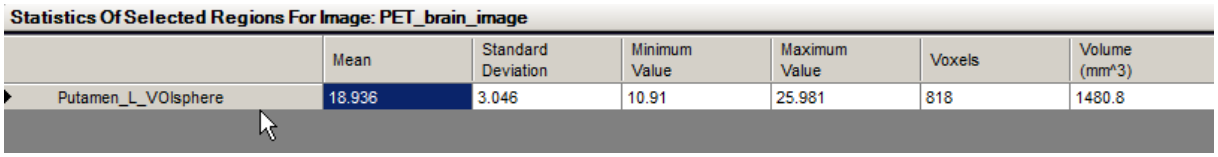
In the right part of the program window the "**Statistics of selected regions…**" table template will appear. The statistics you will get are Mean activity in the region (will be in units of the image), SD, Min-Max values, the number of **Voxels** analysed and the **Volume** of the region.



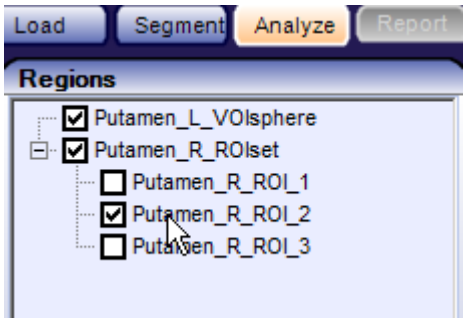
In the Regions panel click on the box of the region you are interested in

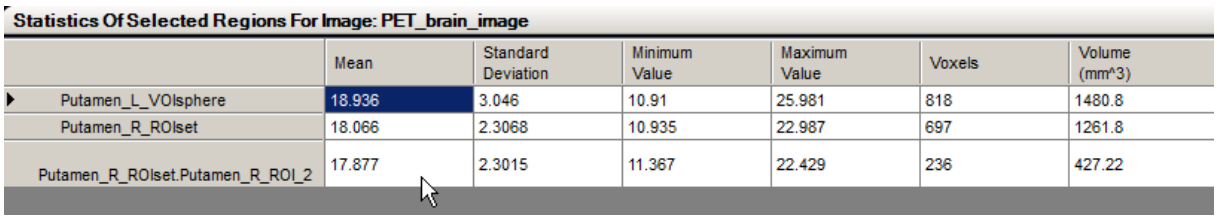


In the "**Statistics…**" table you immediately get the values for that region. As in the example, each VOI will produce one mean value, and the corresponding statistics

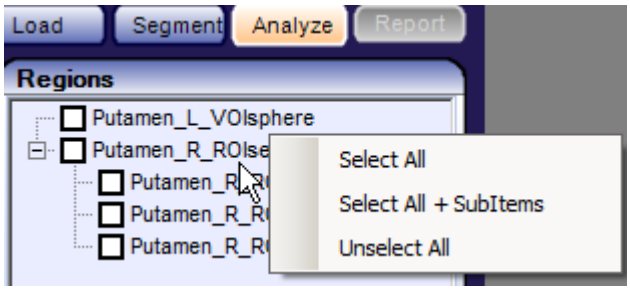


When you analyse a ROI set, you can get the averaged value for the set, as well as values for each of the ROIs drawn



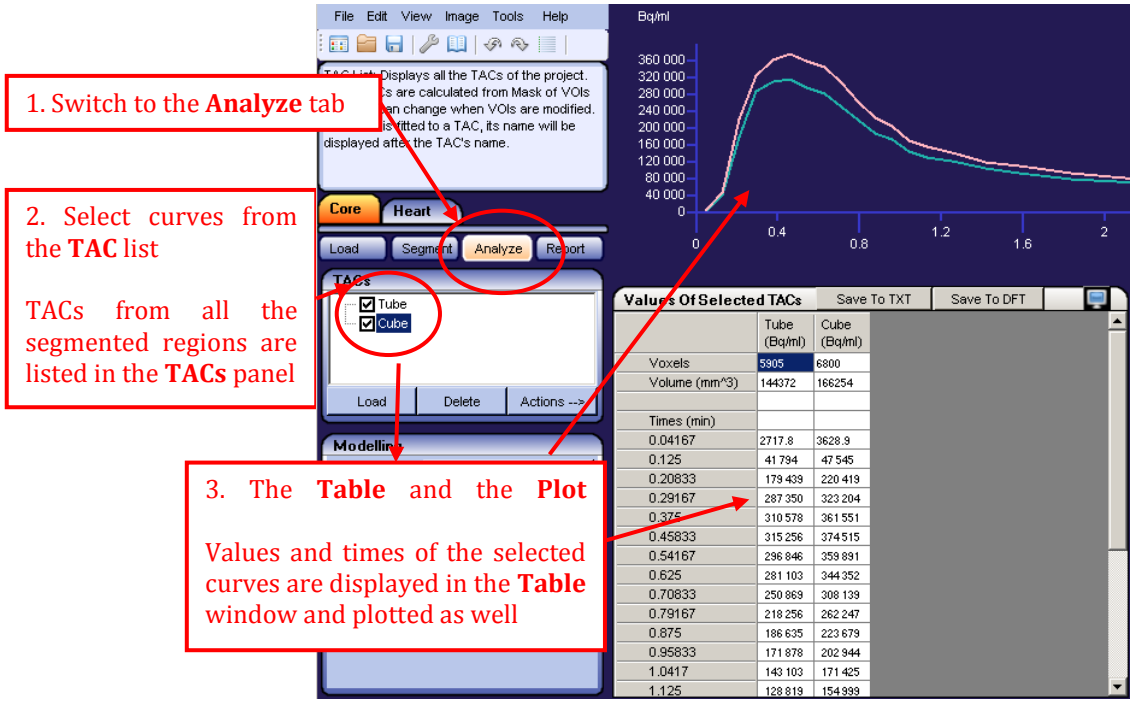


Right-click on the **Regions** panel to select or unselect all regions in the panel.



4.2 Dynamic image analysis

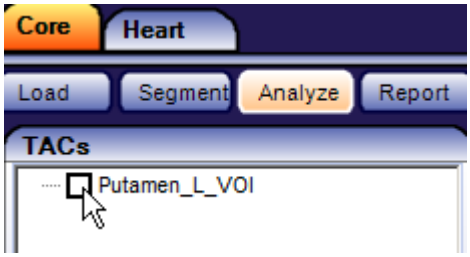
When your main image is a dynamic one, click the **Analyse** tab to get the dynamic analysis view. Curve analysis can be performed in three steps:



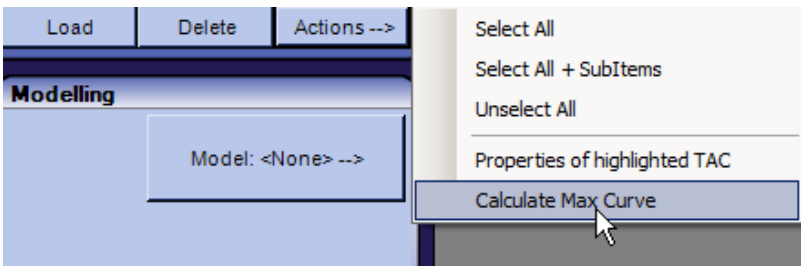
4.2.1 *Calculating 'max' curve*

By default, Carimas calculates TACs by calculating a mean value for each frame. It is also possible to calculate a so-called *'max' curve* by finding a maximum voxel value for each frame.

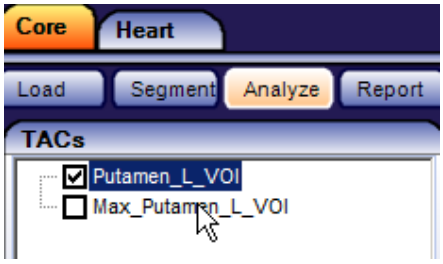
To calculate the 'max' curve, check the box of the needed region's TAC (it should not be loaded from a disk):



Click the **Actions** button and select the **Calculate Max Curve** command

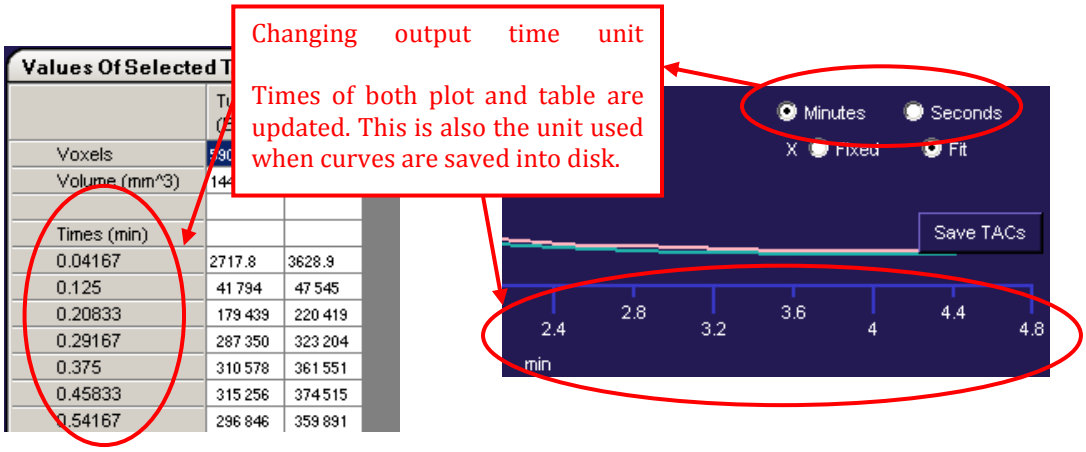


The 'max' curve will be calculated and added to the **TACs** list.



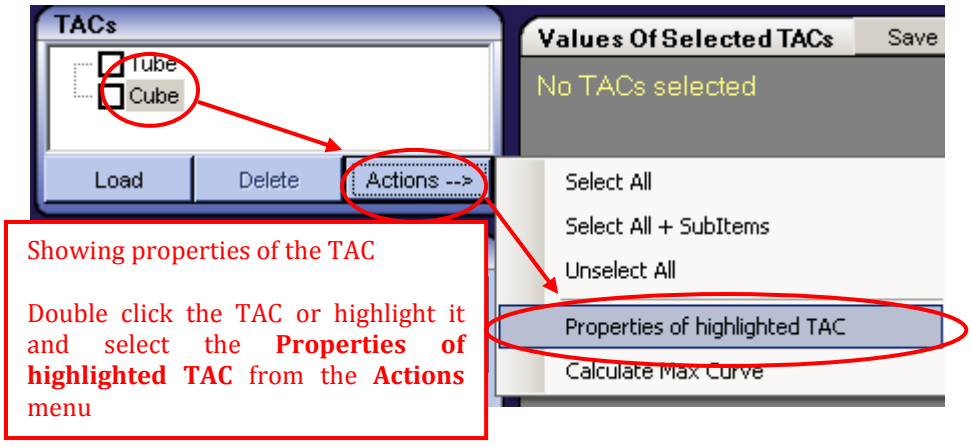
4.2.2 *Changing output time unit*

Output time can be switched between minutes and seconds from top right region of the plot window:

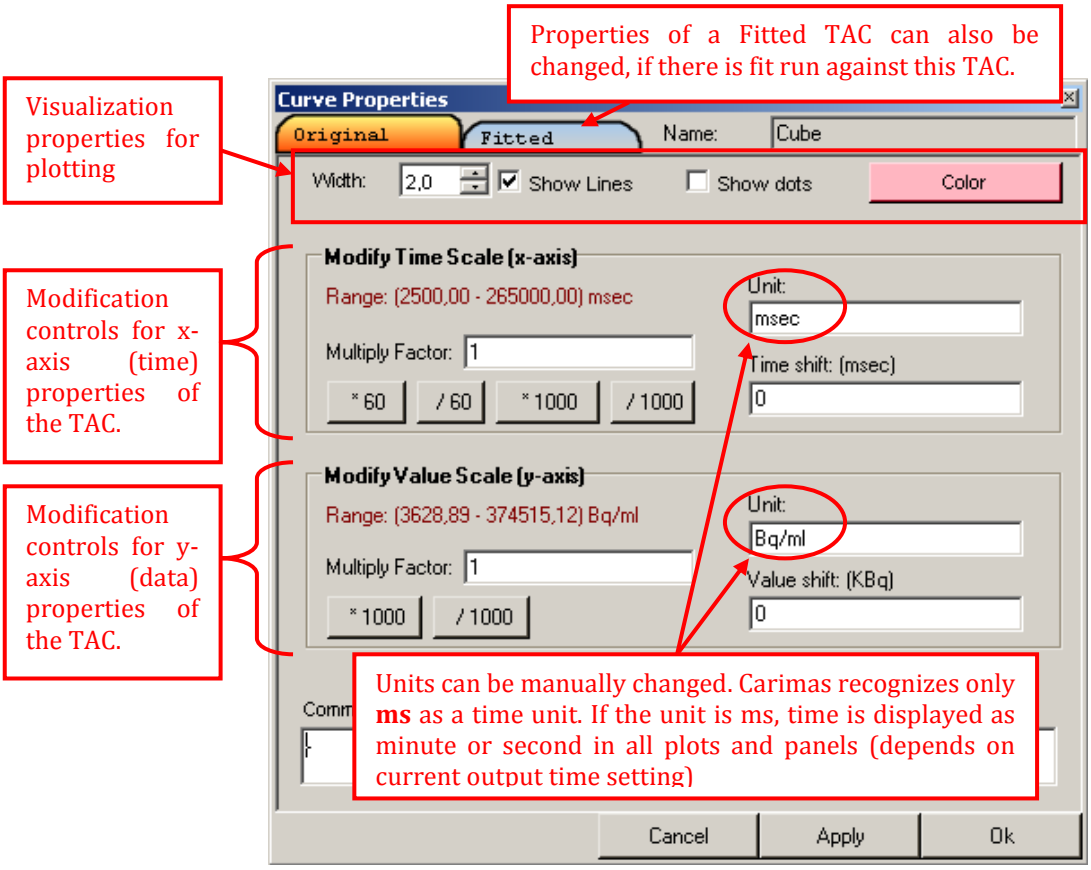


4.2.3 *Curve properties (times, unit, colour, display style)*

Every TAC object has properties that can be modified from the **Curve Properties** dialog box. The box can be opened double clicking the TAC or clicking the **Actions** button:

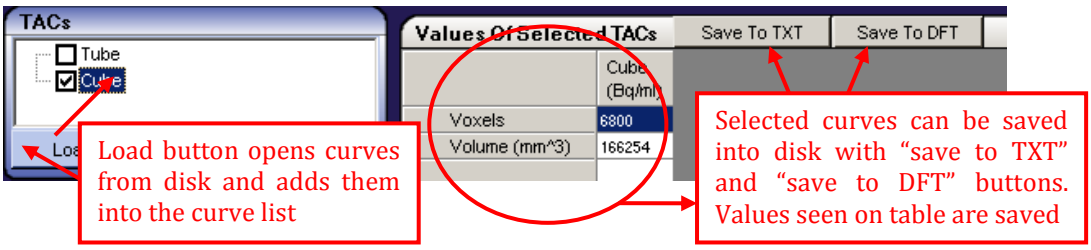


The **Curve Properties** dialog box:



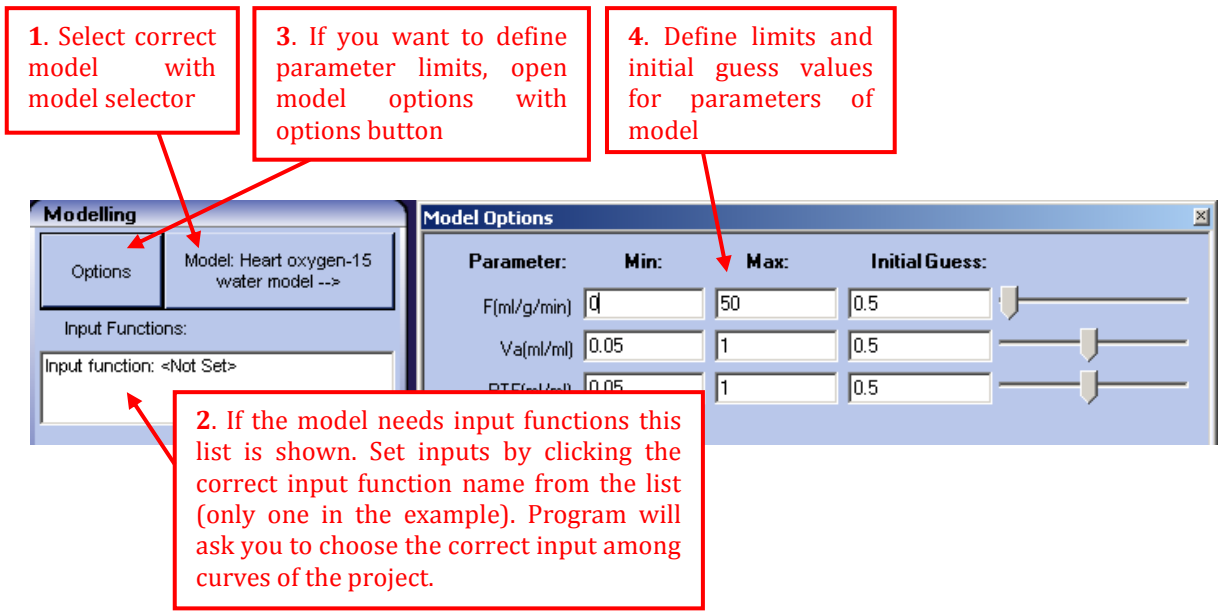
4.2.4 *Loading and saving curves*

Carimas supports loading of external TACs (in DFT) from a disk. TACs can be loaded clicking the **Load** button from the **TACs** panel. Saving is handled from output display windows.

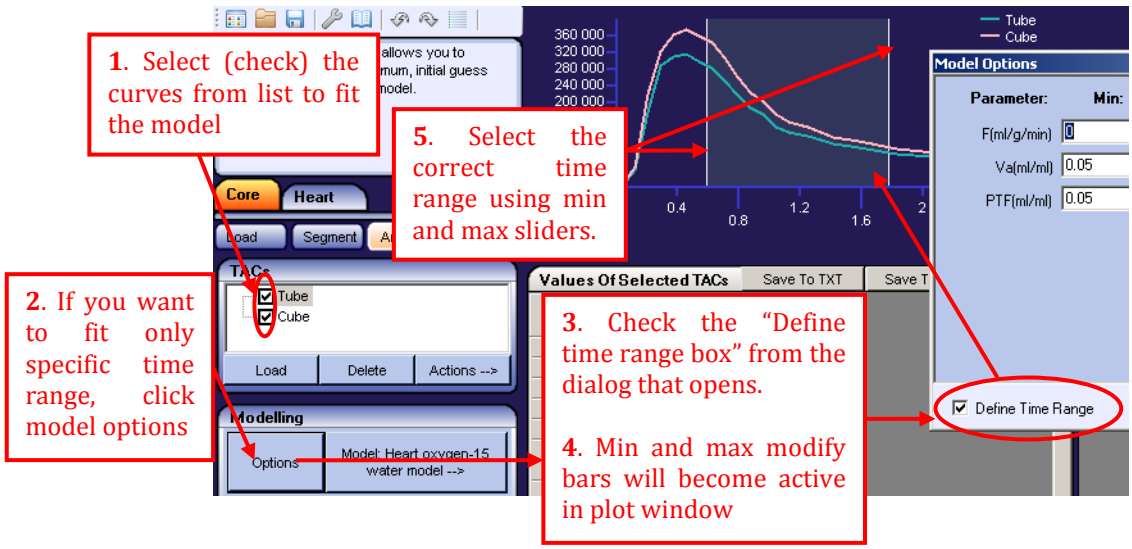

TACs
Tube
Cube
Values Of Selected TACs
Save To TXT
Save To DFT
Cube (Bq/ml)
Voxels
6800
Volume (mm^3)
166254
Load button opens curves from disk and adds them into the curve list
Selected curves can be saved into disk with "save to TXT" and "save to DFT" buttons. Values seen on table are saved

4.2.5 *Modelling (Running a model against a set of TACs)*

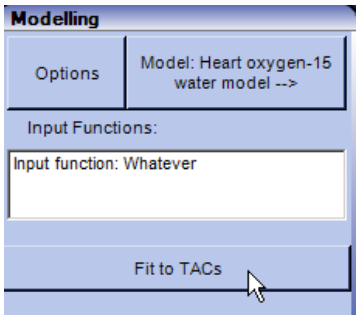
The first step of a modelling process is to select a model and prepare it for the fitting process. The four sub-processes are described in the picture.


1. Select correct model with model selector
3. If you want to define parameter limits, open model options with options button
4. Define limits and initial guess values for parameters of model
Modelling
Options
Model: Heart oxygen-15 water model -->
Input Functions:
Input function: <Not Set>
Model Options
Parameter:
Min:
Max:
Initial Guess:
F(ml/g/min)
Va(ml/ml)
0
50
0.5
0.05
1
2. If the model needs input functions this list is shown. Set inputs by clicking the correct input function name from the list (only one in the example). Program will ask you to choose the correct input among curves of the project.

The second step is to select the TACs to fit and define the modelling time range. The model is fitted separately against all these curves and the best fit curve (and its parameters) is chosen for each TAC. The five sub-processes are in he the picture.

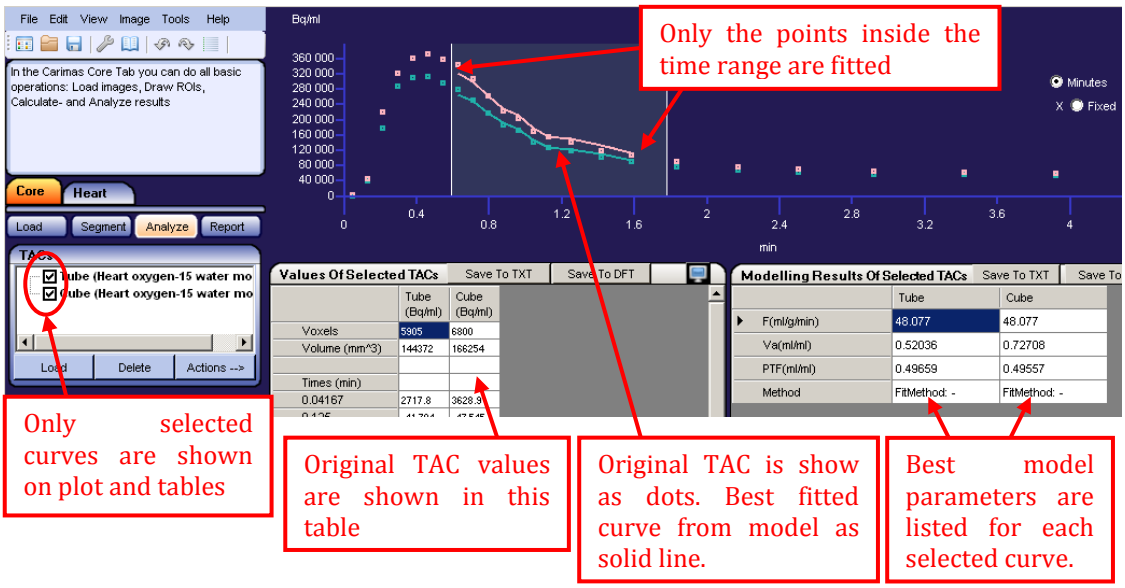


Third step is to run the model. It is done simply clicking the **Fit to TACs** button from model panel



4.2.6 *Inspecting the modelling results*

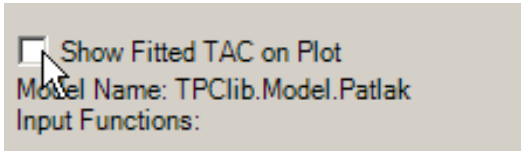
After model is fitted to all selected TACs, the plot will show the fitted curve along with the original curve. Original curve is visualized as dots and fitted curve is a solid line. Modelling results panel will display best parameter values of fitting process for each of the selected TACs.

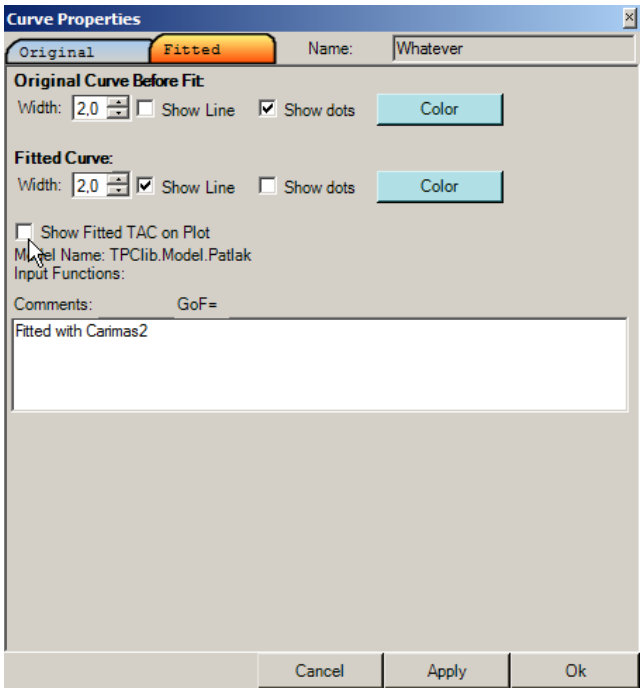

Only the points inside the time range are fitted
Only selected curves are shown on plot and tables
Original TAC values are shown in this table
Original TAC is show as dots. Best fitted curve from model as solid line.
Best model parameters are listed for each selected curve.

It is always possible to do a new fit with different parameters or ranges. Old results will always be overwritten.

4.2.7 *Patlak & Logan with modified time range*

In Patlak and Logan case the running model again with different time range is more tricky because they produce fitted curve with totally different unit and scale than the original curves. After first modelling round the plot will display the patlak / logan plot instead of the original TAC, which will cause time range selector to be in a wrong scale. The easiest way to run the model with different range is simply to undo the last fit and do the fit again. Another way is to uncheck the **Show fitted TAC on plot** checkbox the **Fitted** tab of the **Curve Properties** dialog box.




Curve Properties
Original
Fitted
Name:
Whatever
Original Curve Before Fit:
Width:
2,0
Show Line
Show dots
Color
Fitted Curve:
Width:
2,0
Show Line
Show dots
Color
Show Fitted TAC on Plot
Model Name: TPClib.Model.Patlak
Input Functions:
Comments:
GoF=
Fitted with Carimas2
Cancel
Apply
Ok

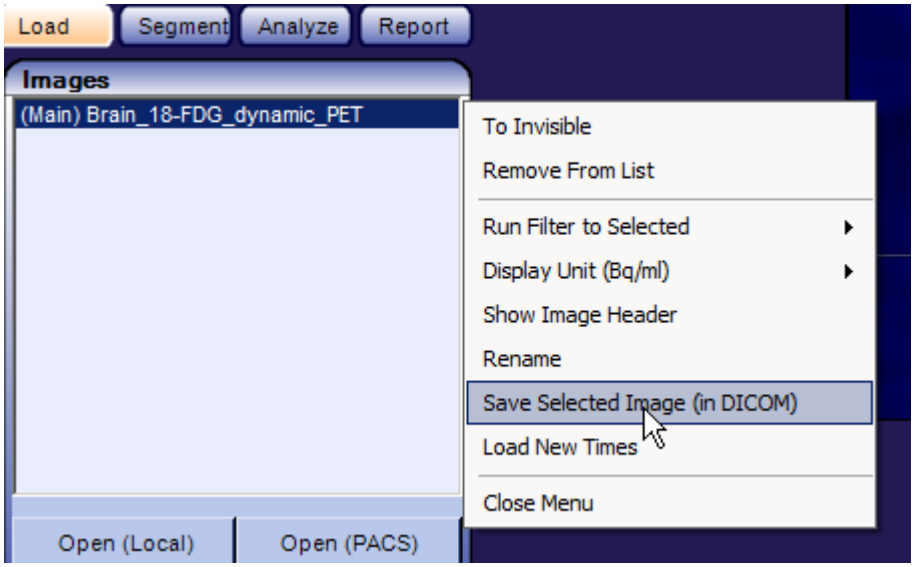
5 Saving and Reporting

All result displaying windows of Carimas have separate buttons for saving data that is displayed on it. Curves are saved from TAC table window, Modelling results from Modelling result table window, Statistics from statistic table window. Plot has button for saving all curves that are currently displayed on it. Also every window can be saved as bitmap file or be printed by using mouse right click context menu

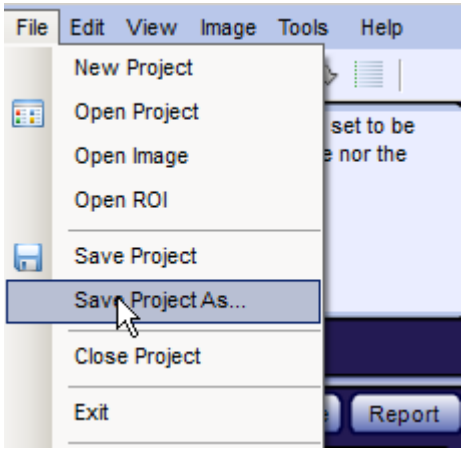
5.1 Saving in Carimas before analysis has been done

You can start saving right after you have downloaded the image into Carimas.

To save the loaded image as DICOM, right-click on the image in the **Images** panel and select **Save Selected Image (as DICOM)**.

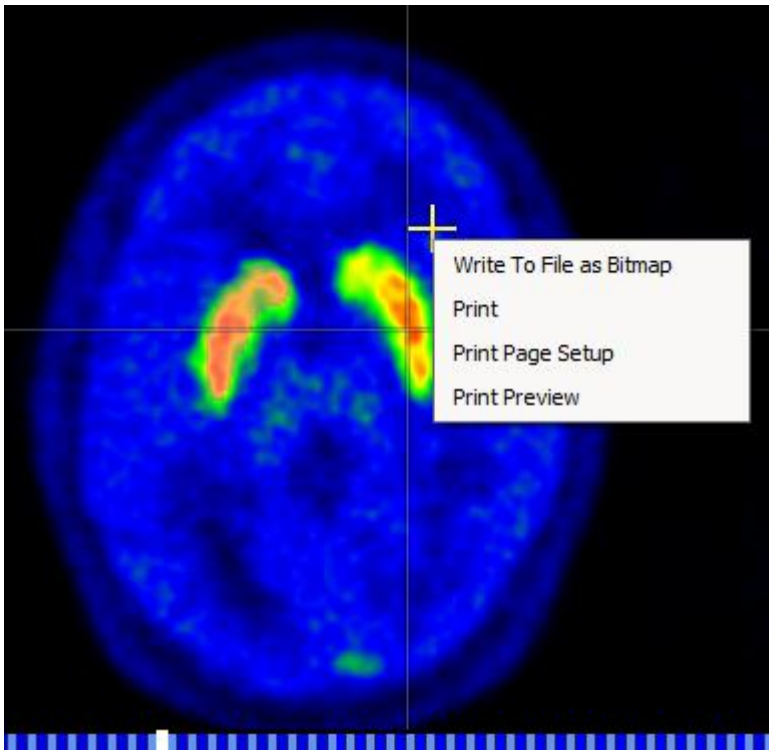


You can save the started project either from the **File** menu:

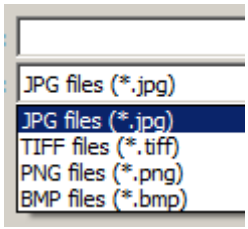


or from the button row:

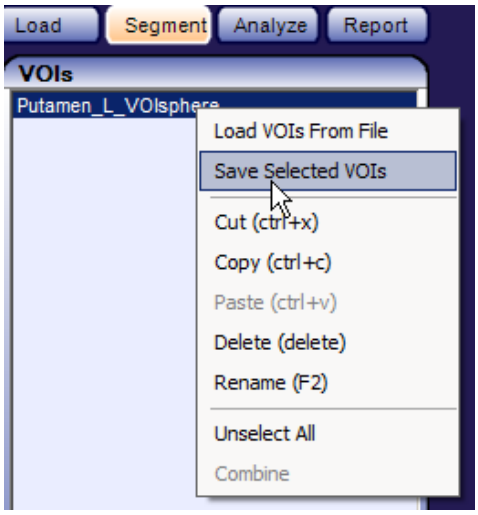
You can save any picture in Carimas (a projection view, a 3D view, a TAC, etc.) at any step of working with the image. Right-click on the image, select **Write To File as Bitmap**

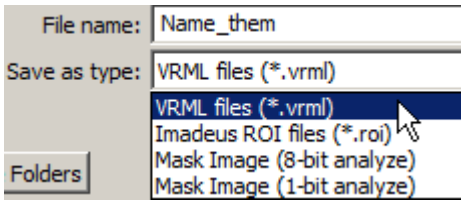


And select from a few publication-friendly image formats:



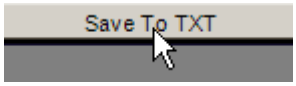
To save the created ROIs/VOIs at segmentation step, select the VOIs, right-click in the **VOIs** panel and select **Save Selected VOIs**.



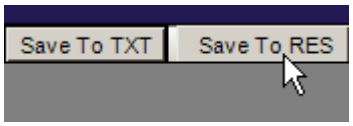


5.2 Saving results of analysis

To save results of a static image analysis click on the **Save To TXT** button near the table with results.



To save the results of a dynamic static analysis, click on **Save To TXT** button to just save modelling results; click on Save To RES to save the modelling results with more information on the modelling method, date of the analysis, etc. Although the Results file has RES extension, it is in the ASCII format, and can be opened by any program opening ASCII files (WordPad, Word, Excel, etc.)

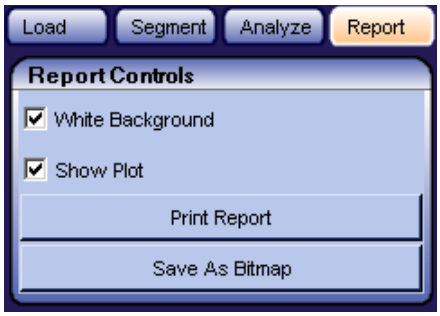


Saving the time activity curve was described earlier.

5.3 Reporting

Carimas has view for showing patient information and dynamic analysis summary in one page report. This view is shown by selecting report tab.

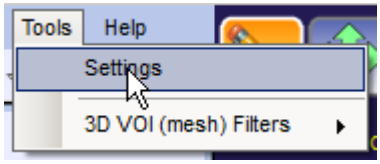
Reports of Carimas can be saved only as bitmap and printed. Carimas will print the report as landscape and fitted to full page. This is done with “Print Report” and “Save as Bitmap” –buttons when report tab is selected.



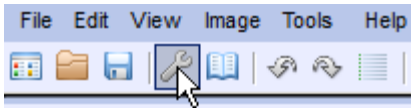
6 Administration

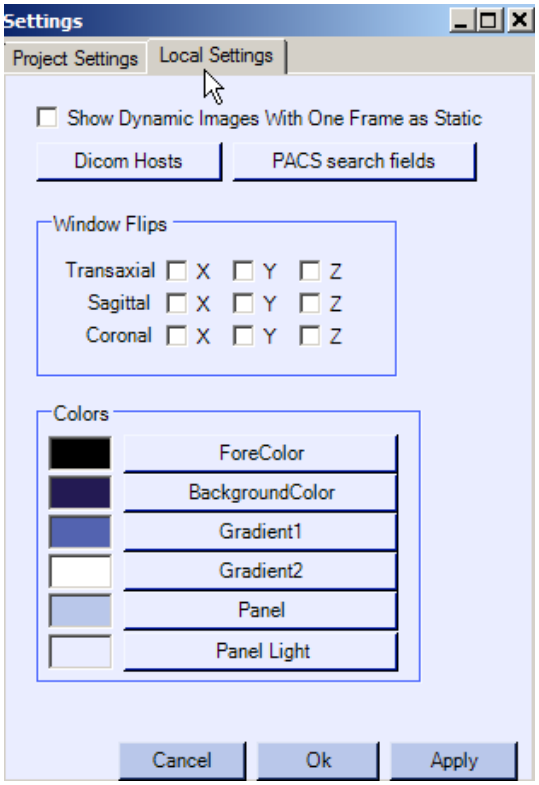
6.1 Local computer settings

PACS server list, PACS search field list and colour schemes are personal settings of the user and are saved under users log in the user account. Personal (i.e. local) settings can be found in the **Local Settings** tab in the **Settings** Panel which can be opened from **Tools** → **Settings**



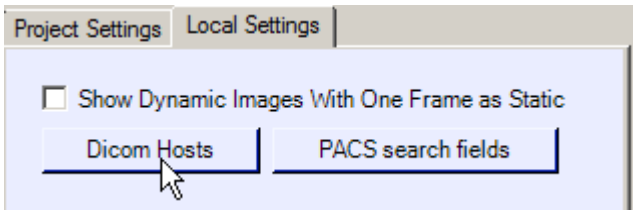
or clicking the **Settings** button:



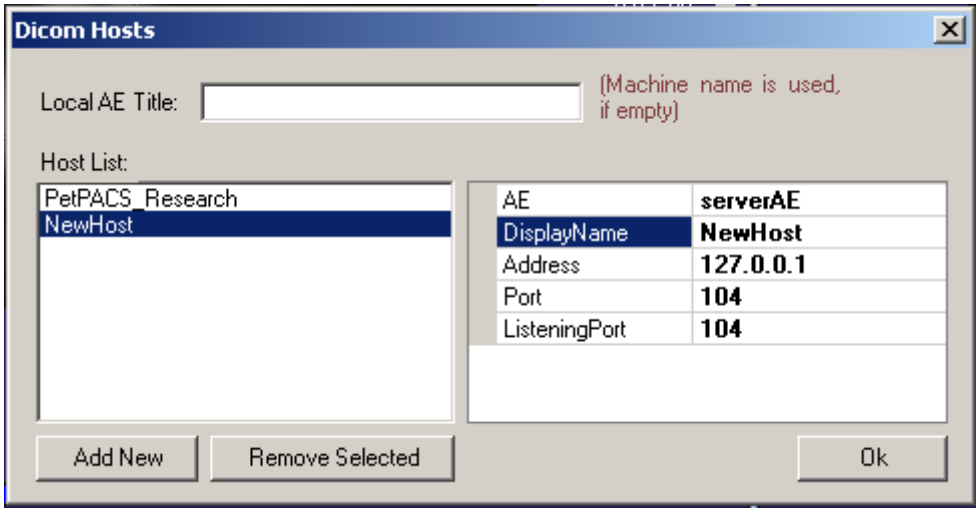


6.1.1 Configuring PACS server list

Servers can be added and removed dynamically from DICOM host panel that opens by clicking the **Dicom Hosts** button:



It opens the **Dicom Hosts** panel:



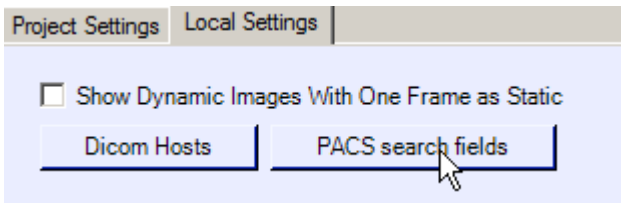
The panel lists all DICOM hosts that exist for the current user. Select the DICOM host in the **Host List** (left) and see properties of this host.

Here you can also define the Application Entity (AE) title of the local client (Carimas machine). If this field is empty, machine's name is used as the AE title.

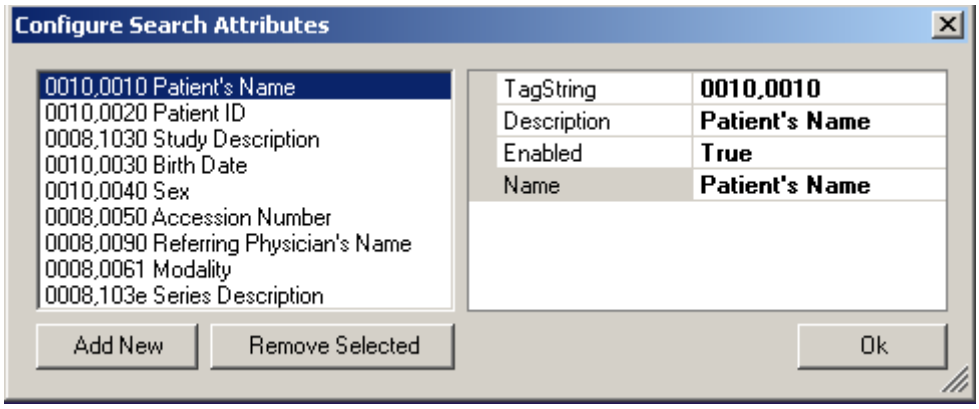
Images are retrieved with C-MOVE, which means that Carimas is a server that the DICOM host is communicating with; therefore needed is the listening port field. IP, AE and port of Carimas client must somehow be defined in a server side for data transfer (Queries will work without).

6.1.2 Configuring PACS search field list

User can make search queries by any DICOM tag. To define the search fields, click the **PACS search fields** button on the **Local Settings** tab page:



It opens the **Configure Search Attributes** panel:



All DICOM search fields are listed on the left. Select an item on the left to see its properties on the right.

The four listed properties are:

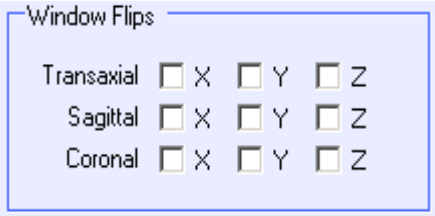
a) **TagString**: The DICOM tag that is used for search query in following hex format: xxxx,xxxx.
b) **Description**: Description text that is shown to user in tool tip when user moves mouse on that search field.
c) **Enabled**: With this flag it is easy to enable and disable search fields, if some server does not allow this DICOM tag or administrator wants to keep the search panel look simple and disable some fields without deleting the whole search tag (enabling is later easy).
d) **Name**: Short caption for filed that is shown in search panel like:

You can add new search field by clicking the **Add New** button,

it creates a new search tag with empty property fields. Fill all the properties and the search field is ready to use.

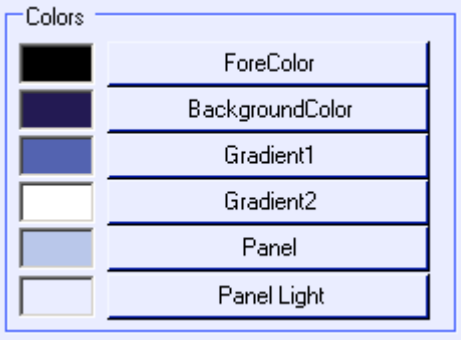
6.1.3 Window flip settings

These settings are exceptional and should be used with caution by an experienced user. The settings let you change the image orientation. They are useful if your image's orientation is wrong, and you want to change it without flipping from the **Image** menu.



6.1.4 *Custom Colours*

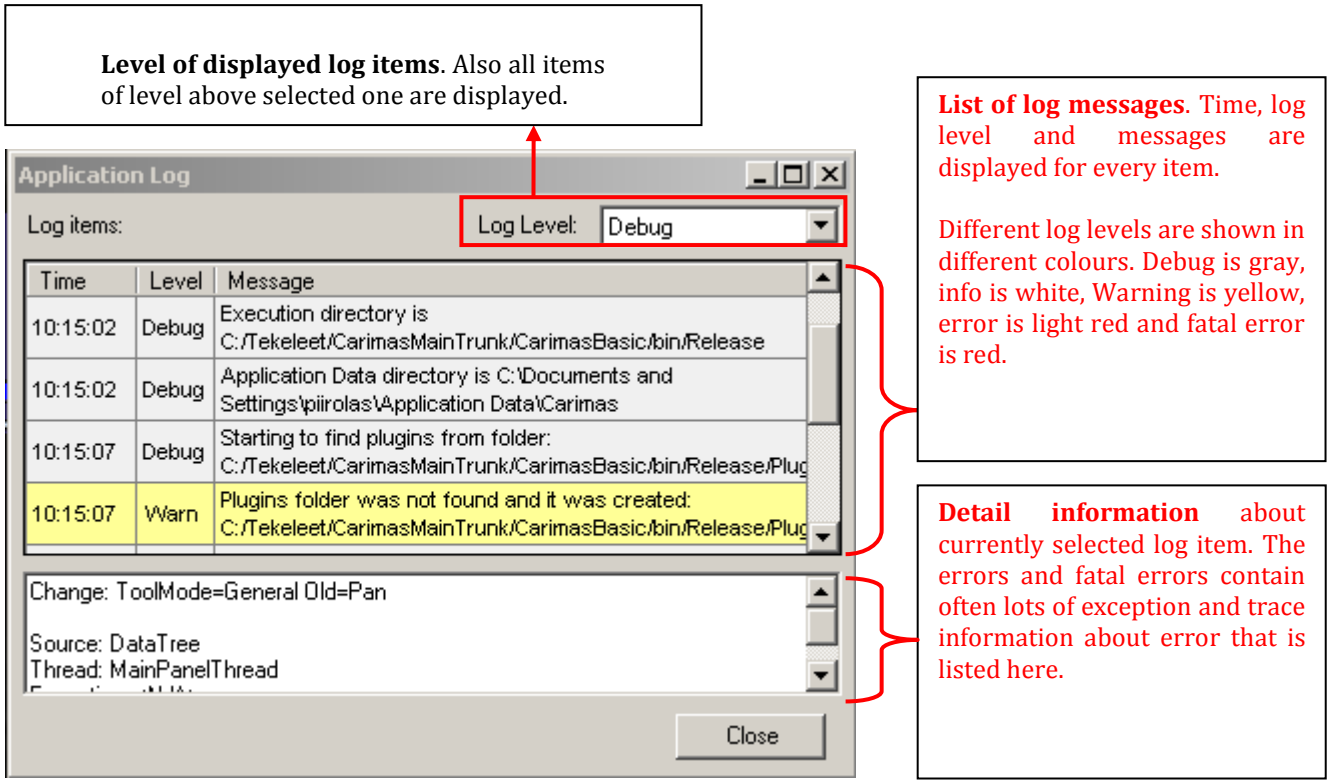
You can customize the colour settings of your Carimas:



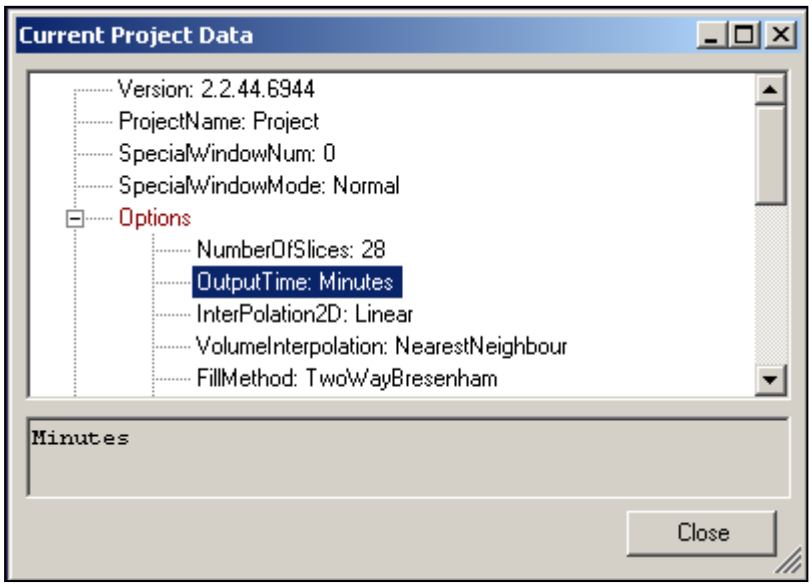
6.2 Application log and error log

Application Log can be opened from **View** → **Log**. All messages of the program are displayed with this component. Log dialog is run separate from other Carimas GUI so that Carimas can be used when log is displayed. Log messages of Carimas are categorized in following five categories:

a) **Debug**: Lowest level and it lists the most detail messages that can be used for tracking errors.
b) **Info**: Message that gives "good to know" information to user.
c) **Warn**: Message if something exceptional was done that user needs to know about. For example if some part of data could not be saved with selected format and were ignored.
d) **Error**: Message that is shown if some command of user was aborted for some reason.
e) **Fatal**: Message when there has been error in program itself. All this kind of errors should be reported as bugs. All errors of this level are automatically written into special error log file that is found from user's personal application data folder.


Level of displayed log items. Also all items of level above selected one are displayed.
Application Log
Log items:
Log Level: Debug
Time
Level
Message
10:15:02 Debug Execution directory is C:/Tekeleet/CarimasMainTrunk/CarimasBasic/bin/Release
10:15:02 Debug Application Data directory is C:\Documents and Settings\piirolas\Application Data\Carimas
10:15:07 Debug Starting to find plugins from folder: C:/Tekeleet/CarimasMainTrunk/CarimasBasic/bin/Release/Plug
10:15:07 Warn Plugins folder was not found and it was created: C:/Tekeleet/CarimasMainTrunk/CarimasBasic/bin/Release/Plug
Change: ToolMode=General Old=Pan
Source: DataTree
Thread: MainPanelThread
Close
List of log messages. Time, log level and messages are displayed for every item.
Different log levels are shown in different colours. Debug is gray, info is white, Warning is yellow, error is light red and fatal error is red.
Detail information about currently selected log item. The errors and fatal errors contain often lots of exception and trace information about error that is listed here.

6.3 Project data viewing



All data currently stored in the project can be seen from selecting View → Project data from menu. Project data dialog will open. The data is categorized in tree structure that can be browsed with panel on top region of the dialog.

The text box on low region of dialog lists the contents of selected node in xml format. This xml is written same way as it will be in the project file xml when the project is saved.

Here user can see and get information that he/she cannot get with normal Carimas GUI, like see or copy point coordinates of some ROI to clipboard, etc…

Glossary

3D volume rendering – the process of reconstructing imaging data from serial consecutive slices in three dimensions for display purposes.

DFT (**D**ata **F**ormat (in) **T**urku) – time-activity curve format used in Turku PET Centre.

DICOM (**D**igital **I**maging and **CO**mmunications in **M**edicine) – a global Information-Technology standard that is used in hospitals worldwide. Its current structure, developed by the National Electrical Manufacturers Association (NEMA) in 1993, is designed to ensure the interoperability of systems used to produce, store, display, process, send, retrieve, query or print medical images and derived structured documents as well as to manage related workflow.

difference image – the result of the *subtraction method* telling which areas in the studied organ are involved in the task state.

dynamic image – reconstructed data of a dynamic scan – a scanning producing several frames of *fixed continuity* – fixed-frame duration (e.g. 6 five-minute frames from 30 to 60 min post-injection) or *variable continuity* – variable frame duration.

ECAT (**E**mission **C**omputed **A**xial **T**omograph) -- a *self-contained* image data format used by the CTI PET scanners.

frame – division of the data matrix that indicates where the image is located in time.

image fusion – a process leading to graphical display of multiparameter data sets representing complex phenomena (e.g. "fusing" MRI data with PET data)

PACS (**P**icture **A**rchiving and **C**ommunication **S**ystem) – electronic systems developed in an attempt to provide economical storage, rapid retrieval of images, access to images acquired with multiple modalities, and simultaneous access at multiple sites". Electronic images and reports are transmitted digitally via PACS.

parametric image – an image that represent both spatial distribution and quantification of the physiological parameters of tracer kinetics.

pixel (short for ***pic****ture* ***el****ement*) – a single point in a graphics image; the smallest element that a device can display and out of which the displayed image is constructed.

plane. The plane is one aspect of an image's matrix. The plane indicates where the image is located relative to the patient's position in the scanner gantry. When a patient is placed in the gantry head first, plane numbers increase in an inferior direction.

plug-in -- a computer program that can, or must, interact with another program to provide a certain, usually very specific, function. Typical examples are plugins to display specific graphic formats (e.g., SVG if the browser doesn't support this format natively), to play multimedia files, to encrypt/decrypt email (e.g., PGP), or to filter images in graphic programs. The main program (a web browser or an email client, for example) provides a way for plugins to register themselves with the program, and a protocol by which data is exchanged with plugins.

polar plot – a schematic representation of myocardium of left ventricle in the form of a segmented circle. Used are 17-segment (AHA) and 20-segment (ASNC) models. Myocardial segments are named and localized with reference to both the long axes of the ventricle and the 360° circumferential locations on the short-axis views.

ROI (Region of interest) -- a contiguous set of pixels in the PET image, defined by hand or automatically, normally used to track radioactivity in the set over time (2D)

self-contained file. A type of file holding not only the original itself but the information about the original – *metadata* (e.g. *.hdr* containing all the acquisition information).

static image – reconstructed data of a static scan – a single-frame acquisition with scanning after the injection.

stress image – an image obtained through a technique for examining the heart's coronary flow reserve by imaging the patient during exercise activity or pharmacologic maneuvers intended to reveal areas of marginal coronary flow reserve caused by partially obstructed regions of the coronaries.

subtraction method – an approach intended to localize the changes in the studied organ. In this approach two different organ (e.g. brain) states are compared: namely, a control state is subtracted from a task state in order to create a *difference image*. This image tells us which areas in the organ are involved in the task state.

VOI (Volume of interest) -- a contiguous set of voxels in the PET image (3D)

voxel (***vo****lumetric pi****xel***) – the three dimensional equivalent of a pixel – a unit of volume corresponding to the smallest element depicted in a three-dimensional image, the signal from which contributes to the intensity of the image.